HUMAN TELOMERASE

		•
60	[GCCC1000010001001001001001001001001001001	ATGCCGCGCGCTCCCCGCTGCC
20	CysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu 2	MetProArgAlaProArgCysA
120	TTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG 12	-
40	nt -u-la-sa-sa-suclumnoClaClumnaralauV=1Gln	STGCTGCCGCTGGCCACGIICG
40	PheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	ValLeuProLeuAlaThrPhe V
		•
180	110000000000000000000000000000000000000	CGCGGGGACCCGGCGGCTTTCC
60	PheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	ArgGlyAspProAlaAlaPheA
		.1.4017.10pr 201——
240	GCCGCCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTG 2	
80	GCCGCCCCCCCAGGTGTCCTGCCTGAAGGACTG	GACGCACGGCCGCCCCCCGGCG
00	AlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	AspAlaArgProProProAlaA
	,	
		•
300	WQQC1Q1QCC1:000000000:1:011:0010010010010010010010	GTGGCCCGAGTGCTGCAGAGGC
100	ArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly 1	ValalaargvalleuGlnArgI
	· · · · · · · · · · · · · · · · · · ·	varianta various in in j-
		_
360		
120	000000000000000000000000000000000000000	TTCGCGCTGCTGGACGGGGCC
120	AlaArgGlyGlyProProGluAlaPheThrThrSerValArg 1	PheAlaLeuLeuAspGlyAlaA
	•	
420	GI CHCCCHCCC ICI CCCCCCCCCCCCCCCCCCCCCCC	AGCTACCTGCCCAACACGGTG2
140	ValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu 1	SarTuri au BroAsnThrVal
		Dell'Alliedi Fordii III (
		_
480		
160	.GAC41001100110011001100110011001	TTGCGCCGCGTGGGCGACGAC
100	AspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal 1	LeuArgArgValGlyAspAsp\
	•	
		•
540	GCCIACCACCICIOCOCCCCCCCCCCCCCCCCCCCCCCCC	CTGGTGGCTCCCAGCTGCGCC
180	AlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla 1	LeuVal Ala ProSerCvsAla
		nedvalAtar 100c10,51120
600	- account careera conservation account conservation for the conservation of the conser	
200	CCGCCACACGCIAGIGGACCCCGALGGGGIGIGGGGIGGG	GCCACTCAGGCCCGGCCCCG
200	oProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu 2	AlaThrGlnAlaArgProPro
660	GICAGGGAGGCCGGGGGGGGGGGGGGGGGGGGGGGGGGG	CGGGCCTGGAACCATAGCGTC
220	valArgGluAlaGlyValProLeuGlyLeuProAlaProGly 2	ArgalaTrpAspHisSerVal
	•	in district bigining of iar
		<u>-</u>
720		•
240	CWGIGCCWCCCMTGIGIGGGGIIGGGGGGGGGGG	GCGAGGAGGCGCGGGGCAGT
240	vSerAlaSerArgSerLeuProLeuProLysArgProArgArg 2	AlaArgArgArgGlvGlvSer

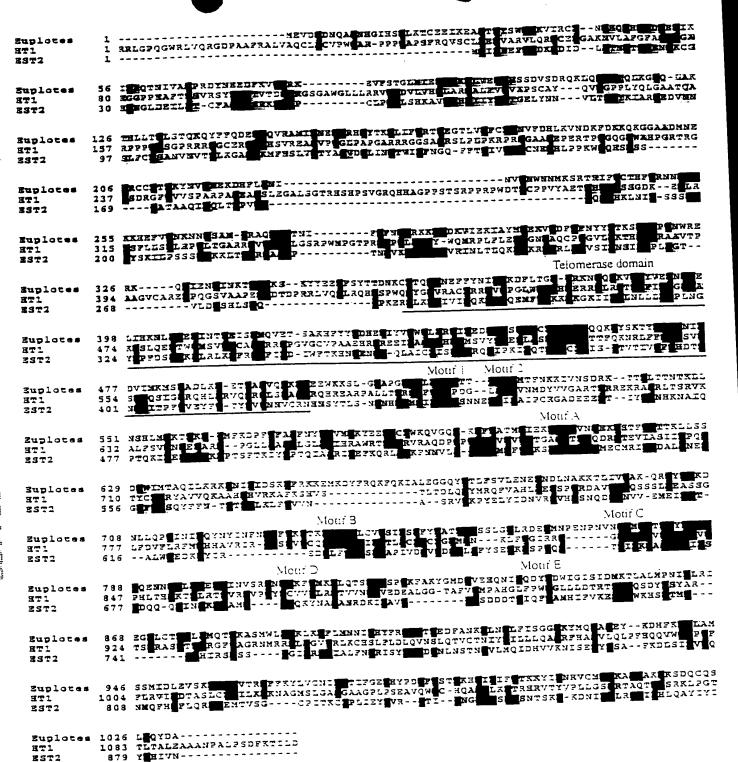
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ariantarioginaloginardinilionardilational distributant a broady	260
AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGTGTCACCTGCCAGACCCGCCGAA	840
ArgThrArgGlyProSerAspArgGlyPheCysValValSerProAlaArgProAlaGlu	280
• • • • • • •	
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GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT	960
	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheleuTyrSerSerGlyAspLysGluGln	340
CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
actually 10001111011041104110411111111111111111	200
	7740
GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC	1140
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	380
• • • • • • • • • • • • • • • • • • • •	
CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
• • • • • • • • • • • • • • • • • • • •	
GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCACC	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG	1320

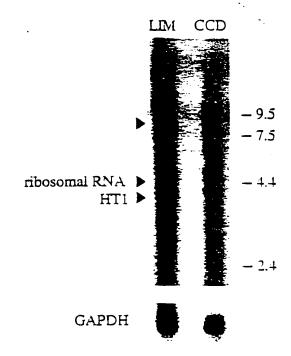
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• • • • • • • • • • • • • • • • • • • •	
GAGGACACAGACCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCACCCCTGGCAG	1380
GluAspThrAspProArgArgLeuValGlnLeuLeuArgGlnHisSerSerProTrpGln	460
• • • • • • • • • • • • • • • • • • • •	
GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC	1440
ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	480
AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT	1500
ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
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							GCTGCGCT1 spCysAla1		1560 520
			•	•	•		•	•	
							IGCGTGAGG		1620
ArgArgS	erPro(SlyValG	LyCysVa	alProAla	AlaGluH	lisArgL	euArgGluG	luIle	540
	•		•	•	•			•	
							IGCTCAGGI		1680
renalal	ysPhel	LeuHlsT	rpLeuMe	etServal	TyrValV	/alGluL	euLeuArgS	SerPhe	560
	•	•	•	•	•		•	•	
							ACCGGAAGA		1740
PuelAin	arrnro	LUTUETI	nrpneGl	LULYSASU	ArgLeur	nePheT	yrArgLysS	serVal	580
	•	•		•	•		•	•	
							IGCAGCTGC		1800
TrpSerL	ysLeuC	InSerI	LeGlyII	LeArgGin	HisLeuL	ysArgV	alGlnLeuA	argGlu	600
	•		• .	•			•	•	
							rgctgacgi		1860
LeuSerG	luAla	SluValAı	cgGlnHi	LsArgGlu	AlaArgP	roAlaLe	euLeuThrS	SerArg	620
	•	•	•	•	•		•	•	
							rggactace		1920
renarge	uerre	roLysri	COASPGI	-yreuarg	brollev	alAsnMe	etAspTyrV	alval	640
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							CGAGGGTGA		1980
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							rgggcgcci		2040
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	•	-	•	•	•		•	•	
							STGTGCGGG		2100
LeuGIYL	euAspA	AspIleHi	LsArgAl	.aTrpArg	IhrPheV	alLeuAı	rgValArgA	laGln	700
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	•	•		•	•		•	•	
							GCAAGGCCI		2280
vaıArgA	rgTyrA	⊔aValVa	ITGTUTA	salaalai	alsGlyH	ısValAı	gLysAlaF	heLys	760

·	2340
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SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	700
	2400
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GlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu	800
GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC	2460
GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACGCACG	820
AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	020
-	
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ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	040
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CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGCGCTACAGCTGTTTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGCGCGACATGGAGAACAAGCTGTTTTGCGCGAGAACAAGCTGTTTTGCAGCTGTTTTTTTT	860
LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	300
GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGACACCTCACCTCACCCCACGCG	2640
GGGCTGCTCCTGCGTTTGGTGGATGATTTCTTGTTGGTGATCACCTCTGTTGTTGGTGATCACCTCTGTTGTTGGTGATCACCTCTGTTGTTGGTGATCACCTCTGTTGTTGGTGATCACCTCTGTTGTTGGTGATCACCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	880
GlyLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	000
•	
AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGTGAACTTG	2700
AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCTGAGTCCCTCAGTCTCAGTCCTCAGTCCTCAGTCCTCAGTCCTCAGTCCTCAGTCCTCAGTCTCAGTCCTCAGTCTCAGTCCTCAGTCCTCAGTCCTCAGTCCTCAGTCCTCAGTCCTCAGTCCTCAGTCAG	900
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	200
•	
CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT	2760
CGGAAGACAGTGGTGAACTTCCCTGTAGACACTCCCTGTAGACTCCTGTAGACTCTGTAGACTAGACTCTGTAGACTCTGTAGACTCTGTAGACTCTGTAGACTCTGTAGACTAGACTCTGTAGACTCTGTAGACTA	920
ArgLysThrValValAsnPheProValGluAspGluAlaLeuGlyGlyThrAlaPheVal	,20
CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG	2820
CAGATGCCGGCCCACGGCCTATTCCCCCCCCCCCCCCCC	940
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuLeuAspThrArgThrLeu	2
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GAGGTGCAGAGCGACTACTCCAGGCTATACTACTACTACTACTACTACTACTACTACTACTACT	960
GluValGlnSerAspTyrSerSerTyrAlaArgThrSerIleArgAlaSerLeuThrPhe	•
AACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTG	2940
AACCGCGGCI ICAAGGCIGCAAAAAAAAAAAAAAAAAAA	980
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AAGTGTCACAGCCTGTTTCTGGATTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAAC	3000
LysCysHisSerLeuPheLeuAspLeuGlnValAsnSerLeuGlnThrValCysThrAsn	1000
rAscAsurase trentuere member engineering arrange transfer and a research	
	2000
ATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCA	3060
IleTyrLysIleLeuLeuGlnAlaTyrArgPheHisAlaCysValLeuGlnLeuPro	1020
TIGIALDASIIGNEGNEGOT:	

TTTCATCAGCAAGTTTGGAAGAACCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCC PheHisGlnGlnValTrpLysAsnProThrPhePheLeuArgValIleSerAspThrAls	3120 1040
£11011720711041111	
	3180
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC	1060
TCCCTCTGCTACTCCATCCTGAAAGCGTAGTAGGTAGGTA	1000
	3240
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GCCGCCGGCCCTCTGCCCTCCGAGCCGTCGTTTTTPLeuCysHisGlnAlaPheLeuLeuAlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	2000
AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG	3300
AAGCTGACTCGACACCGTGTCACCTACGTGCCACTGCTGGGGTGTGTGT	1100
LysLeuThrArgHisArgValintiyiValitobealedeljeetta	
ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCCTGACTGCCCTGGAGGCCGCAGCCAAC	3360
ACGCAGCTGAGTCGGAAGCTCCCGGGGGTGGTTGTTCTTTTTTTT	1120
IntGinLeuSelArguyo2011111	
	2420
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACtgatggccacccgcccacagccag	3420 1132
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132
	3480
Geegagageagacaceageagecetgtcacgeegggetetacgtcccagggagggagggg	3540
a	3600
	3660
	3720
	3780
	3840
	3900
gtgtgccctgtacacaggcgaggaccccgcactatatatgagtttttcagttttgaaaaaaa ggggggaggtgctgtgggagtaaaatactgaatatatgagtttttcagttttgaaaaaaa	3960
	3964
aaaa	





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FIG. 3

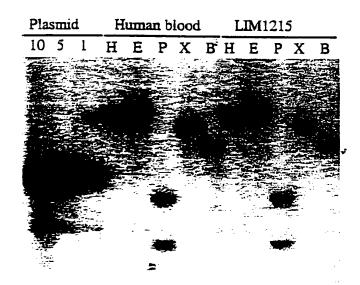


FIG. 4

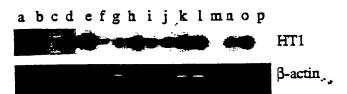


FIG. 5



FIG. 6

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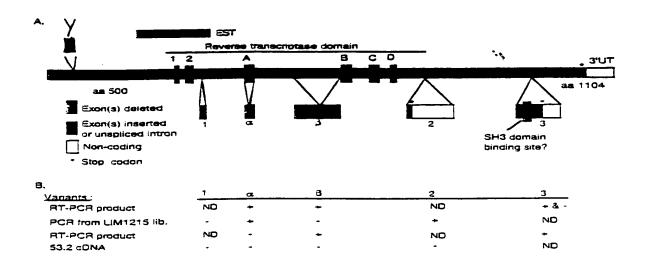


FIG. 7A and 7B

223 222 gcaggtg|TCCTGCC-3' 5'-CCAGGTG|ggcctc 1952 5'-AAAGAGG|GTGCCTG......AACAGAA|GCCGAGC-3' 2130 5'-TGTCAAG|gtggatg.....cccccag|GACAGGC-3' 5'-GAGCCAC|gtctcta.....ggggcaa|GTCCTAC-3' 5'-ACTCCAG|GTCAGCG.....XXXXXXX|CTATGCC-3' TAAEEMILVVTPAVLGSGQPEME PPRRPSGVGSPPVSPGRGVG 3158 CCCTCCCCCTCTCACCCCTCTCTTTTCCCCCACIGGATGTC-3' L G L *

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FIG. 7C



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FIG. 8

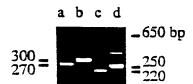


FIG. 9

sequence "Y" 104-105 bases

GGCCTCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCCGGCGGGGGAACCAG GlyLeuProGlyValGlyValArgLeuGlyLeuArgAlaAlaGlyGlyAsnGln AlaSerProGlySerAlaSerGlyTrpGly * GlyArgProGlyGlyThrSer ProProArgGlyArgArgProAlaGlyValGluGlyGlyArgGlyGluProAla

CGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG ArgHisAlaGluSerSerAlaGlyAspSerGlyArgPheProArgArg AspMetArgArgAlaAlaGlnAlaThrGlnGlyAlaSerProAlaGly ThrCysGlyGluGlnArgArgArgLeuArgAlaLeuProProGlnVal

sequence "1" 38 bases

GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAA ValAlaValLeuTrpPheAsnPheLeuPheAsnGlnLys

sequence "a" 36 bases

GTGGATGTGACGGGCGCGTACGACACCATCCCCAG ValAspValThrGlyAlaTyrAspThrIleProGln

sequence "\$" 182 bases

GTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTG ValSerThrLeuThrAspLeuGlnPrcTyrMetArgGlnPheValAlaHisLeu

CAGGAGACCAGCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGGInGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeu

AATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCAC AsnGluAlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHis

GCCGTGCGCATCAGGGGCAA AlaValArgIleArgGlyLys

partial sequence "2" unknown length

GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCAG
Ter

GGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGT CAGATGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTG TGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA...

sequence "3" 159 bases

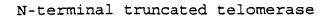
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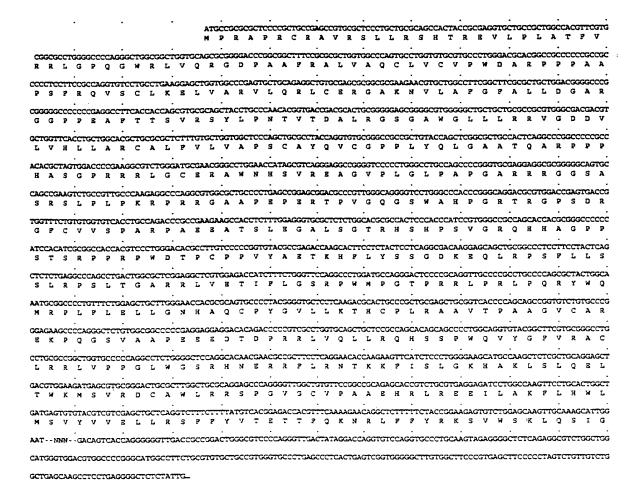
 $\label{thm:proproblem} \textbf{ATGGAGCCACCCGCAGACCGTCGGGTGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGMetGluProProArgArgProSerGlyValGlySerPheProValSerProGlyArg$

GGAGTTGGGCTGGGCCTGTGACTCCTCAGCCTCTGTTTTCCCCCAGGlyValGlyLeuGlyLeu *

sequence "X" unknown length

partial sequence of genomic intron (approximately 2.7 kb)
GTGGCTGTGCTTTGGTTTAACTTCCTTTTTAACCAGAAGTGCGTTTGAGCCCCACATT
TGGTATCAGCTTAGATGAAGGGCCCGGAGGAGGGGCCACGGGACACAGCCAGGGCCAT
GGCACGGCGCCCCACCCATTTGTGCGCACAGTGAGGTGCCGAGGTGCCGCACAGGGAAAAGCAGCGTGGGGGTGTAGGGGGAGCTCCTGGGGCAGGGAC....





Truncated protein 1

M P R A P R C R A V R S L L R S H T R B V L P L A T P V CCCCCCTGGGCCCCAGGGCTGGCGGCTGGTGCAGCGCGGGACCCGGGGCTTTCCGGGGGCTGGTGGCCCAGTGCTGTGTGGGGTGCCCTGGGACGCACGGCCGCCCCCCGGG RRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDARPPPAA CCCCTCCTTCCGCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGCCTGCGAGCGCGCGGAGAACAGTGCTGGCCTTCGGCTTTCGCCTTGCTGGACGGGCCCG S F R Q V S C L K B L V A R V L Q R L C S R G A K N V L A F G F A L L D G A R G P P E A P T T S V R S Y L P M T V T D A L R G S G A W G L L L R R V G D D V GCTGGTTCACCTGCTGCACGCTGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGGGCCCAGCTGGGGGCGGCGGCTGTACCAGCTCGGGGCTGCCACTCAGGCCCGGCC VHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPP ACACCCTACTGGACCCCGAAGGCCTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGGGGCCCGGGGTCCCCTGGGCCTGCCAGGCCCCGGGTGCGAGGAGGAGGCCCGGGGGCAGTGC S R S L P L P K R P R R G A A P B P B R T P V G Q G S W A H P G R T R G P S D R G F C V V S P A R P A E E A T S L B G A L S G T R H S H P S V G R Q H H A G P W D T P C P P V Y A B T K H P L Y S S G D K E Q L R P S P L L S S L R P S L T G A R R L V Z T I P L G S R P W M P G T P R R L P R L P Q R Y W Q ANTICOGCCCCTOTTTCTGCAGCTGCTTGGGAACCACGCGCAGTGCCCCTTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTGCCAGCAGCCGGTGTCTGTGCCCG M R P L P L B L L G N H A Q C P Y G V L K T H C P L R A A V T P A A G V C A R GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCGAGGAGGAGGAGACACAGACCCCCGTCGCCTGGCAGCTGCTCGCCAGCAGCAGCAGGTGTACGGCTTCGTGGGGGCCTG EKPQGSVAAPZZZDTDPRRLUQLLRQHSSPWQVYGFVRAC L R R L V P P G L W G S R H N B R R F L A N T K K F I S L G K H A K L S L Q E L GACGTGGAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCCAGGGGTTGGCTTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCATGGCTT W K M S V R D C A W L R R S P G V J C V P A A B H R L R E E I L A K F L H W L GTGGCTGTGCTTTGGTTTAACTTCCTTTTTTAACCAGAA

V A V L W F T F L F N Q K

Truncated protein 2

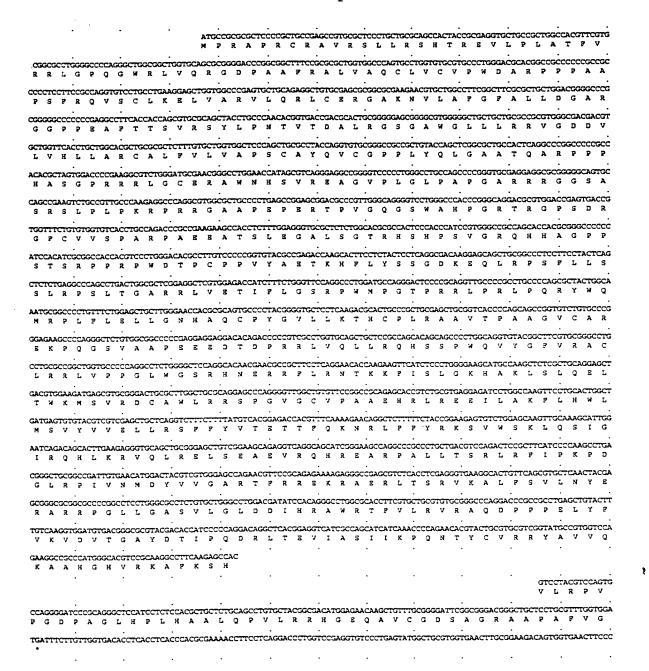


FIG. 11C

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Reference protein

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG	60
MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	20
GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCCTGGGGGCCCCAGGGCTGGCGGCTGGTGCAG	120
ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	40
Aginedi i Operata i i i i i i i i i i i i i i i i i i	
CGCGGGGACCCGGCGGCTTTCCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGC	180
ArgGlyAspProAlaAlaPheArgAlaLeuValAlaGlnCysLeuValCysValProTrp	60
ArgGIYASpProAlaAlaPheArgAlaDedValAlaGinGyDDedValGyDJU	•
GACGCACGGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	240
GACGCACGGCCGCCCCCCGCCGCCCCCCCCCCCCCCCC	80
AspAlaArgProProProAlaAlaProSerPheArgGlnValSerCysLeuLysGluLeu	80
	300
GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGCG	
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
	2.50
TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCCGAGGCCTTCACCACCAGCGTGCGC	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGGGGGGGG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
Deuvarrationerey Shrary Lorin. 42-97-42-7	
GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA	600
AlaThrGlnAlaArgProProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu	200
AlainiGinalaargproproproprionisalaseldiyiloong.ug.ugsudgudoiyoyodu	200
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT	660
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCGGGGTC	220
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
	720
GCGAGGAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGT	720
AlaArgArgArgGlyGlySerAlaSerArgSerLeuProLeuProLysArgProArgArg	240
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GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
AGGACGCGTGGACCGAGTGACCGTGGTTTCTGTGTGGTGTCACCTGCCAGACCCGCCGAA	840
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GAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTCCCACCCA	900
GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
CGCCAGCACCACGCGGGCCCCCCATCCACATCGCGGCCACCACGTCCCTGGGACACGCCT	960
ArgGlnHisHisAlaGlyProProSerThrSerArgProProArgProTrpAspThrPro	320
ALGORIMISMISMISMISMISMISMISMISMISMISMISMISMIS	
TGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTCAGGCGACAAGGAGCAG	1020
CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
CysFloFloVallylAlaGldInillyshist.nezed1,1-0-0-0-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	
CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC	1080
LeuArgProSerPheLeuLeuSerSerLeuArgProSerLeuThrGlyAlaArgArgLeu	360
neuwidatopelauenennengelgetnenwidatopelneniutgivargwiduen	200
GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC	1140
GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGACTCCCCGCAGGTTGCCC	380
ValGluThrIlePheLeuGlySerArgProTrpMetProGlyThrProArgArgLeuPro	٥٥٥
	1000
CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC	1200
ArgLeuProGlnArgTyrTrpGlnMetArgProLeuPheLeuGluLeuLeuGlyAsnHis	400
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GCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGCTGCGAGCTGCGGTCACC	1260
AlaGlnCysProTyrGlyValLeuLeuLysThrHisCysProLeuArgAlaAlaValThr	420
FIC 11D	

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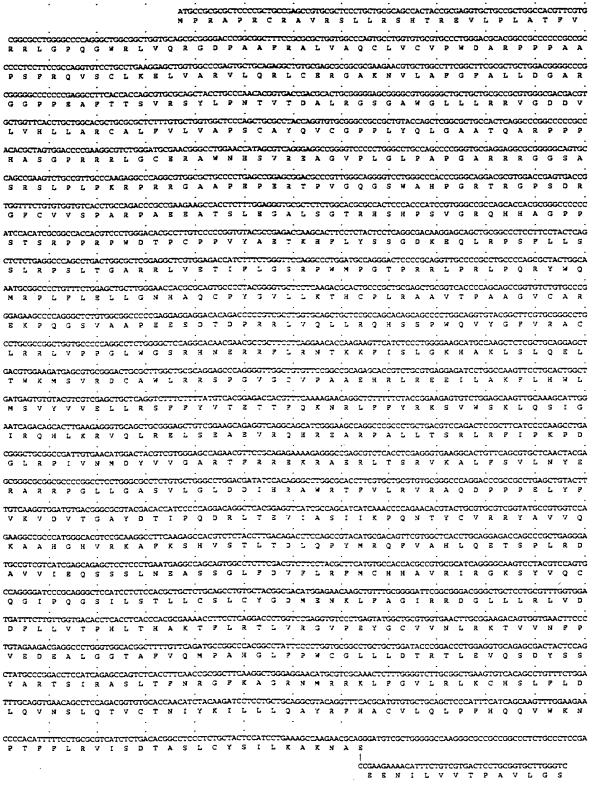
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GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	1440 480
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ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPheIleSerLeuGlyLysHis	500
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AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	520
CGCAGGAGCCCAGGGGTTGGCTGTTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC	1620
ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	540
$\tt CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC\\ LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe$	1680 560
${\tt TTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTC} \\ {\tt PheTyrValThrGluThrThrPheGlnLysAsnArgLeuPhePheTyrArgLysSerVal} \\ {\tt Constant} \\ {\tt Co$	1740 580
TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG	1800
TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	600
CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCC	1860 620
CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG	1920
LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	640
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GlyAlaArgThrPheArgArgGluLysArgAlaGluArgLeuThrSerArgValLysAla	660
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GACCCGCCGCCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATC AspProProProGluLeuTyrPheValLysValAspValThrGlyAlaTyrAspThrIle	2160 720
CCCCAGGACAGGCTCACGGAGGTCATCGCCAGCATCATCAAACCCCAGAACACGTACTGC	2220
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SerHisValSerThrLeuThrAspLeuGlnProTyrMetArgGlnPheValAlaHisLeu	780
CAGGAGACCAGCCCGCTGAGGGATGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGlnGluThrSerProLeuArgAspAlaValValIleGluGlnSerSerSerLeuAsnGlu	2400 800
GCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC AlaSerSerGlyLeuPheAspValPheLeuArgPheMetCysHisHisAlaValArgIle	2460 820
AGGGGCAAGTCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTG ArgGlyLysSerTyrValGlnCysGlnGlyIleProGlnGlySerIleLeuSerThrLeu	• • • • • • • • • • • • • • • • • • • •
CTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGATTCGGCGGGAC LeuCysSerLeuCysTyrGlyAspMetGluAsnLysLeuPheAlaGlyIleArgArgAsp	
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GlyLeuLeuLeuArgLeuValAspAspPheLeuLeuValThrProHisLeuThrHisAla	880
AAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGAACTTG	2700
LysThrPheLeuArgThrLeuValArgGlyValProGluTyrGlyCysValValAsnLeu	900
CGGAAGACAGTGGTGAACTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTT	2760
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CAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTG	2820
GlnMetProAlaHisGlyLeuPheProTrpCysGlyLeuLeuAspThrArgThrLeu	940
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	2100
TCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGC SerLeuCysTyrSerIleLeuLysAlaLysAsnAlaGlyMetSerLeuGlyAlaLysGly	3180 1060
	2240
GCCGCCGGCCCTCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTC AlaAlaGlyProLeuProSerGluAlaValGlnTrpLeuCysHisGlnAlaPheLeuLeu	3240 1080
AAGCTGACTCGACACCGTGTCACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCCAG LysLeuThrArgHisArgValThrTyrValProLeuLeuGlySerLeuArgThrAlaGln	3300 1100
ACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGCAGCCAAC ThrGlnLeuSerArgLysLeuProGlyThrThrLeuThrAlaLeuGluAlaAlaAlaAsn	3360 1120
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CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC ProAlaLeuProSerAspPheLysThrIleLeuAsp	3420 1132
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Truncated protein 3

M P R A P R C R A V R S L L R S H T R E V L P L A T F R R L G P Q G W R L V Q R G D P A A P R A L V A Q C L V C V P W D A R P P P A A CCCTTCTTTCCGCCAGGTGTCCTGCAGGAGCTGGTGGCCCGAGTGCTCCAGAGGCTGTGCGGAGAAAACGTGCTGGCCTTCGGCTTCGGCTGCTGGACGGGGCCCG PSFRQVSCLKELVARVLQRLCERGAKNVLAFGFALLDGAR G G P P B A F T T S V R S Y L P N T V T D A L R G S G A W G L L R R V G D D V LVHLLARCALPVLVAPSCAYQVCGPPLYQLGAATQARPPP ACACGCTAGTCGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGGGGGAAGTGC HASG'PRR LGC BRAWN HSV RBAG V PLG L PAPGARR GGS A CAGCCGAAGTCTGCCCTAGAGGGCCCAGGCGTGGCGCTGCCCCTGAGCCGGAGCGCCGTTGGGCAGGGGTTCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG S R S L P L P K R P R R G A A P E P B R T P V G Q G S W A H P G R T R G P S D R G P C V S P A R P A R B A T S L B G A L S G T R H S H P S V G R Q H H A G S T S R P P R P W D T P C P P V Y A B T K H P L Y S S G D K E Q L R P S P L L S $\tt ctctctaaggccctaactggggctcgaaggctcgtagagaccatctttctaggttccaggccctagatgccaggactccccgcaggttgccccagcgctactggca$ L R P S L T G A R R L V B T I P L G S R P W M P G T P R R L P R L P Q R Y W Q ANTICOGCCCCTOTTCTCGAGCTOCTTCGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGGTCACCCCAGCAGCCGGTGTCTCTGTGCCCG M R P L P L B L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R E K P Q G S V A A P E E S D T D P R R L V Q L L R Q H S S P W Q V Y G F V R A C L R R L V P P G L W G S R H N E R R ? L R N T K K ? I S L G K H A K L S L Q E L IRQHLKRVQLRELSEAEVRQHREARPALLTSRLR?IPKPD $\tt COGGCTOCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA$ G L R P I V N M D Y V V G A R T P R R Z K R A E R L T S R V K A L P S V L N Y E RARRGLLGAS V L G L D D I H RAW R T P V L R V R A Q D P P P E L Y P TOTCAAGOTGGATGTGACGGGGCGTACGACACCATCCCCCAGGACAGGCTCACGGAGGACACCATCATCACAACACCATCATCAGAACACGTACTGCGTACGGTGCGTACGGTGCGTCCA K V D V T G A Y D T I P Q D R L T E V I A S I I K P Q N T Y C V R R Y A V V V V I E Q S S L N E A S S G L F D V F L R F M C H H A V R I R G K S Y V Q C CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACAACAAGCTGTTTCGGGGGGATTCGGGGGACGGGCTGCTCTGCGTTTTGGTGGA Q G I P Q G S I L S T L L C S L C Y G D M B N K L P A G I R R D G L L R L V D TGATTTCTTGTGGACACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATATGGCTGGTGAACATTGCGGAAGACATGGTGAACATTCCC T P H L T H A K T P L R T L V R G V P B Y G C V V N L R K T V V N P P TOTAGAAGACGAGGCCCTGGGTGGCACGCCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGGTGGATACCCGGACCCTGGAGGGTGCAGAGCGACTACTCCAG B D B A L G G T A P V Q M P A H G L P P W C G L L L D T R T L E V Q S D Y S R GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCTGCCAAGCGCCGTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA

Altered C-terminus protein



AATACTGAATATATGAGTTTTTCAGTTTTGA

ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG PRAPRCRAVRS LLRS HTREVLPLAT coecsectes secret secP Q G W R L V Q R G D P A A F R A L V A Q C L V C V P W D A R P P P A A S F R Q V S C L K S L V A R V L Q R L C B R G A K N V L A P G F A L L D G A R G G P P E A P T T S V R S Y L P N T V T D A L R G S G A W G L L R R V G D D V GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCGGCCCCCGCCC LVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPP HASGPRERLGCBRAWNHSVEBAGVPLGLPAPGARRGGSA S R S L P L P K R P R R G A A P E P B R T P V G Q G S W A H P G R T R G P S D R G P C V V S P A R P A B B A T S L B G A L S G T R H S H P S V G R Q H H A G P P STSRPP A PW D T P C P P V Y A B T K H P L Y S S G D K E Q L R P S F L L S CTCTCTGAGGCCCAGCCTGACTGGCGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTTCCCCCGCAGGTTGCCCCAGCGCTACTGGCA S L R P S L T G A R R L V B T I F L G S R P W M P G T P R R L P R L P ANTICOGCCCCTGTTTCTGGGGCTCCTTGGGAACCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCCTTGCGGGTCACCCCAGCAGCCGGTGTCTGTGCCCGMM R P L F L Z L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R GGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTGGAGGTGTCCGCCAGCACAGCACAGCACCCCTTGGCAGGTGTACGGCTTCGTGCGGGCCTT EKPQGSVAAPEEEDTDPRRLVQLLRQHSSPWQVYGFVRAC L R R L V P P G L W G S R H N S R R P L R N T K K P I S L G K H A K L S L Q S L GACGTGGAAGATGAGCGTGCGGGACTGCGCAGGAGCCCAGGGGTTGGCTGTGCTCGCCCAGAGCACCCGTTGGGAGGAGTCCTGGCCAAGTTCCTGCACTGGGT T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K P L H W L GATGAGTGGTACGGCGCCCCAGGTCTTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAGGAGAGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V B L L R S F F Y V T S T T F Q K N R L F F Y R K S V W S K L Q S I G AATCAGACAGCTTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCTGCTGACGTCCAGACTCCGCATCATCCCCAAGCCTGA I R Q H L K R V Q L R E L S E A E V R Q H R E A R P A L L T S R L R F I P K P D CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA G L R P I V N M D Y V V G A R T P R R E R R A E R L T S R V K A L P S V L N Y E R A R P G L L G A S V L G L D D I H R A W R T F V L R V R A Q D P P P S L Y F TGTCAAG DRLTEVIASIIKPQNTYCVRRYAVVQ GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACACGTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG AVVIEQSSSLNEASSGL? D7 ? LR? MCHHAVRIRGKSYVQC CEAGGGGATCCCGCAGGGTTCCATCCTCCACGCTGCTCTGCAGCCTGTGCTACGCGGGACATGGAGGACAAGCTGTTTGCGGGGATTCGGCGGACGGGCTGCTCTGCGTTTTGGTGGA Q G I P Q G S I L S T L L C S L C Y G D M E N K L P A G I R R D G L L R L V D TGATTTCTTGTTGGTGACACCTCACCCCACGCGAAAACCTTCCTCAGGACCCTCGTCCGAGGGTGTCCCTGAGTATGGCTGCGTGAACTTGCGGAAGACAGTGGTGAACTTCCCC D P L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N P TOTAGAAGAGGGGCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG V E D E A L G G T A F V Q M P A H G L F P W C G L L D T R T L E V Q S D Y S CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCCCGGCTTCAAGGCT3GGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGACTGAAGTGTCACAGCCTGTTTCTGGA Y A R T S I R A S L T F N R G F K A G R N M R R K L F G V L R L K C H S L F L. D TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCAGTTTCATCAGCAAGTTTGGAAGAA L Q V N S L Q T V C T N I Y K I L L L Q A Y R P H A C V L Q L P P H Q Q V W T P F L R V I S D T A S L C Y S I L K A K N A G M S L G A K G A A G P L P GGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGCTGACTCGACACCGTGTCACCTACGTGCCACTCTGGGGTCACTCAGGACAGCCCAGACGCAGACGCTGAGTCGGAAGCTCCC V Q W L C H Q A F L L K L T R H R V T Y V P L L G S L R T A Q T Q L S R K L P G T T L T A L E A A A N P A L P S D 7 K T I L D CAGTGTCCGGCTGAGCCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGACTCCACCCCAGGGCCAGGCTTTTCCTCAC CAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAA GGACCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAA ATGCCCCGCCTCCCCGCTSCCGAGCCGTGCGCTCCCTGCTGCGGAGCCACTACCGCGAGGTGCTGCCGCCACGTTCGTG

RAPRCAAVRSLLRSHTREVLPLATFV CGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAGCGGGGGACCCGGGGGCTTTCCGGGGGCCTGGTGGCCCAGTGCGTGGGGTGGCCTGGGACGCACGGGCCGCCCCCGGCGC R R L G P Q G M R L V Q R G D P A A P R A L V A Q C L V C V P M D A R P P P A A PS F R Q V S C L K E L V A R V L Q R L C E R G A K N V L A P G P A L L D G A R TSVRSYLPNTVTDALRGSGAWGLLLRRVGDD GCTGGTTCACCTGCTGGCACGCTGCTGCGGCTCCTTTGTGCTGGTCGCTCCCAGCTGCGCCTTACCAGGTGTGCGGGCCGCCGGCTGTACCAGCTGGGCGCTGCCACTCAGGCCCGGCCCCGGCC H L L A R C A L P V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P HASGPRRELGCBRAWNHS V REAGVPLGLPAPGARRGGSA RSLPLPKRPRRGAAPERTPVGQGSWAHPGRTRGPSDR G P C V V S P A R P A B B A T S L B G A L S G T R H S H P S V G R Q H H A G P P ST S R P P R P W D T P C P P V Y A B T K H P L Y S S G D K E Q L R P S P L L S CTCTCTGAGGCCCAGCCTGACTGGGGGCCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCCCGCAGCCCTACTGGCA L R P S L T G A R R L V B T I F L G S R P W M P G T P R R L P R L P Q R Y M Q M R P L P L B L L G N A A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R GENGANGCCCCNGGGCTCTGTGGGGGCCCCCGGAGGAGGACACAGACCCCCGTGGCCTGGTGCAGGTGCTCCGCCAGCAGCAGCAGCAGCAGCAGGAGGTGTTACGGCTTCGTGCGGGGCCTG E K P Q G S V A A P E E E D T D P R R L V Q L L R Q H S S P W Q V Y G P V R A C L R R L V P P G L W G S R H N B R R P L R N T K K P I S L G K H A K L S L Q E L WKMSVRDCANLRRSPGV3CVPAAEHRLREEILAKFLHWL AATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAGCTGTCGGAAGCAGAGCTCAGCAGCAGCACAGCAGCAGCCTGCGGAGCCTGCAGACGTCCAGACTTCATCCGCAAGCCTGA I R Q H L K R V Q L R Z L S E A Z V R Q H R E A R P A L L T S R L R F I P K P D CGGGCTGCGGCGATTGTGAACATGGACTACGTCGTGGGAGCCAAACGTTCCGCAGAAAAAAGAGGCGGCGAGCGTCTCACCTCGAGGGTGAAGACTGTTCAGCGTGAACTACGA G L R P I V N M D Y V V G A R T P R R B K R A E R L T S R V K A L F S V L N Y E GCGGCCGCGCCCCCGCCTCTGGGCCGCCTCTGTGCTGGGCCTCGGCCTTGGACGATATCCACAGGGCCTGGCGCACTTTCGTGCTGCTGTGCGGGCCCAGGACCCAGGACCCCGGCCTGAGCTGTACTT RARRPGLLGASVLGLDD: BRAKRTFVLRVRAQDPPPELYF TGTCAAG v K GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATCAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG A V V I E Q S S S L N B A S S G L ? D V ? L R ? M C H H A V R I R G K S Y V Q C CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACCACGCCACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA Q G I P Q G S I L S T L L C S L C Y G D M E N K L F A G I R R D G L L R L V D TGATTTCTTGTTGGTGACACCTCACCCCACCCGAAAACCTTCCTCAGGACCCTTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGGAACTTGCGGAAGACAGTGGTGAACTTCCC D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T EDEAL G G T A F V Q M P A H G L 7 P W C G L L L 3 T R T L E V Q S D GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCACGTGCTGCTGCTGCCGCGCTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA

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FIG. 11.J

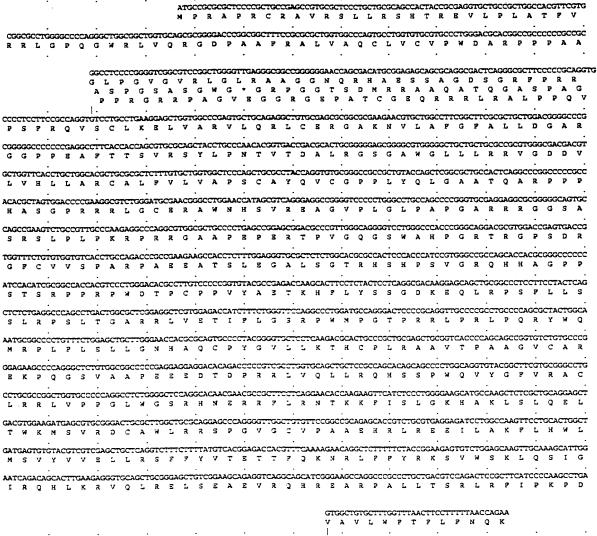
TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTGGTAA

M P R A P R C R A V R S L L R S H T R E V L P L A T F R R L G P Q G W R L V Q R G D P A A P R A L V A Q C L V C V P W D A R P P P A A S F R Q V S C L K E L V A R V L Q R L C B R G A K N V L A F G F A L L D G A R G G P P S A P T T S V R S Y L P N T V T D A L R G S G A W G L L L R V G D D V GCTGGTTCACCTGCTGGCACGCTGCGCGCCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCCTACCAGGTGTGCGGCCCGCCGCTGTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCGCCC LVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPP H A S G P R R L G C E R A W N H S V R B A G V P L G L P A P G A R R G G S CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGGCGGTGCCCCTGAGCCGGAGCGGAGCGCGTTGGGCAGGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG RSLPLPKRPRRGAAPEPBRTPVGQGSWAHPGRTRGPSDR V S P A R P A E E A T S L E G A L S G T R H S H P S V G R Q H H A G P P ST S R P P R P W D T P C P P V Y A Z T K H P L Y S S G D K E Q L R P S F L L S CTCTCTGAGGCCCAGCCTGACTGGGGGGCTCGGGGGGGCCATGGAGCCCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGGCGGGGGTTGCCCCAGCGCTACTGGCA S L R P S L T G A R R L V E T I P L G S R P W M P G T P R R L P R L P Q R Y W AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCGGTGCGGGTCACCCCAGCAGCGGGTGTCTGTGCCCG
M R P L F L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R GAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAGGAGGACACAGACCCCCGTCGCCTGGTCGACCTCCTCCCCCAGCACAGCACCCCCTGGCAGGAGGTGTACGGCTTCGTGCGGGGCCTG EKPQGSVAAPEEEDTDPRRL7QLLRQHSSPWQVYGFVRAC L R R L V P P G L W G S R H N E R R P L R N T K K F I S L G K H A K L S L Q E L GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCACGGGTTTGGCTTGTTTCCCGCCGCAGAGCACCCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT TWKMSVRDCAWLRRSPGVGCVPAAEHRLREEILAKFLH R Q H L K R V Q L R E L S E A Z V R Q H R E A R P A L L T S R L R F I P K P D G L R P I V N M D Y V V G A R T F R R Z K R A E R L T S R V K A L F S V L N Y E V L G L D D I H R A W R T F V L R V R A Q D P P P E L Y RARRPGLLGAS TGTCAAG DRLTEVIASIIK PQNTYC V RRYA GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG AVVIEQSSSLNEASSGL FD V FLR FM CH H AVRIRGKS Y V Q C CCAGGGGATCCCGCAGGGCTCCATCCTCCCACGCTGCTCTGCAGCCTGTGCTACGCGCACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA Q G I P Q G S I L S T L L C S L C Y G D M 3 N K L F A G I R R D G L L R L V D TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGGTGTCCCTGAGTATGGCTGCGTGAACTTGCGGAAGACAGTGGTGAACTTCCC D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N F TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGGAGCCCTGGAGGTGCAGAGCGACTACTCCAG E D E A L G G T A P V Q M P A H G L ? P W C G L L D T R T L E V Q S D Y S S ARTSIRASLT FNRGFKAGRNMRRKL FGVLRLKCHSL FLD TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA LQVNSLQTVCTNIYKILLQAYRFHACVLQLPFHQQVWKN FLRVISDTASLCYSILKAKN CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC

GGGACAGCCAGAGATGGAGCCACCCCCCAGACCGTCGGGTGTGGGCAGCTTTCCGGTGTCTCCTGGGAGGGGAGTTGGGCTGTGACTCCTCAGCCTCTGTTTTCCCCCAG
G Q P E M E P P R R P S G V G S P P V S P G R G V G L G L *

EENILVVTPAVLGS

M P R A P R C R A V R S L L R S H T R B V L P L A T F V RLGPQGWRLVQRGDPAAPRALVAQCLVCVPWDARPPPAA G L P G V G V R L G L R A A G G N Q R H A B S S A G D S G R F P R R A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G P P R G R P A G V B G G R G B P A T C G E Q R R R L R A L P P Q V CCCCTCCTTCCCCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGGGCGCGAAGAACGTGCTGGCCTTCGGCTTCGGCTGCTGGACGGGGCCCG PSPRQVSCLKBLVARVLQRLCBRGAKNVLAPGPALLDGAR LVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARPPP HASGPRREGCERAWN HSVREAGVPLGLPAPGARRAGGSA CAGCCGAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTTGCCCCTGAGCCCGAGCGGAGCGCCCGTTGGGCAGGGGTCCTGGCCCACCCGGGCAGGACGCGTTGACCGAGTGACCG S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R G P C V V S P A R P A B B A T S L B G A L S G T R H S H P S V G R Q H H A G P P TSRPPRPWDTPCPPVYABTKHFLYSSGDKEQLRPSFLLS LRPSLTGARRLVBTIFLGSRPWMPGTPRRLPQRYWQ ANTICOGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCGCTGCGAGCTGCGTGACCCCAGCAGCAGCCGGTGTCTGTGCCCG M R P L P L B L L G N H A Q C P Y G 7 L L K T H C P L R A A V T P A A G V C A R GGAGAAGCCCCAGGGCTCTGTGCCGCCCCCGAGGAGGAGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCCCCAGCAGACAGCAGCCCCTGGCAGGTTGTACGGCTTCGTGCGGGCCTG EKPQGSVAAPESEDTOPRRLVQLLRQHSSPWQVYGFVRAC GACGTGGAACATGACCGTGCGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTTGTGTTTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT WKMSVRDCAWLRRSPGVJCVPAAEHRLREEILAKFLHWL GATGAGTGTTACGTCGTCGAGCTGCTCAGGTCTTTCTTTTATGTCACGGAGCACGTCTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGGTGTCTGGAGCAAGTTGCAAAGCATTGG
M S V Y V V Z L L R S F F Y V T E T T F Q K N R L F F Y R K S V W S K L Q S I G CATGGGTGGACGTGGCCCCGGGGATGGCCTTCTGCGTGTGCGTGGGTGCCCTGAGCCCTCACTGAGTCGGTGGGGGCTTGTGGCTTCCCGTGAGCTTCCCCCTAGTCTGTTTTTCTG GCTGAGCAAGCCTCCTGAGGGGGCTCTCTATTG_



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ATGCCGCGCTCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTCGTG M P R A P R C R A V R S L L R S H T R B V L P L A T F R R L G P Q G W R L V Q R G D P A A P R A L V A Q C L V C V P W D A R P P P A A GGCTTCCCCGGGTTCGGCTTCGGGTTGAGGGCGGCGGGGGAACCAGCGACATGCGGAGAGCAGCGACTCAGGGGGCTTCCCCCGCAGGTG L P G V G V R L G L R A A G G N Q R H A B S S A G D S G R F P R R S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G P R G R P A G V B G G R G B P A T C G B Q R R R L R A L P P Q V PSFRQVSCLKELVARVLQRLCBRGAKNVLAFGFALLDGAR G G P P B A P T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V GCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTGCTGGGGCTCCCAGCTGGCGCTACCAGGTGTGCGGCCCCCGCTGTACCAGCTCGGGGCTGCCACTCAGGCCCGGCCCCGGCC LVHLLARCALPVLVAPSCAYQVCGPPLYQLGAATQARPP ACACCCTAGTCCCCCAAGCCTCTGGATCCGAACGGCCTGGAACCATACCTTCAGGAGGGGGCCTGGGTCCCCTGGCCAGCCCGGGTCCGAGGAGGAGGCGCGGGGGAATGC HASGPRRELGCERAWN HSV REAGVPL GLPAPGARR GGSA CAGCCGAACTCTCCCCTAGACGCCCAGGCGTGCCCTTGCCCTTGAGCCGAGCCGTTGGGCAGGGTCCTGGGCCCACCCGGGCAGGACGCGTGGACCGAGTGACCG S R S L P L P K R P R R G A A P E P E R T P V G Q G S W A H P G R T R G P S D R G P C V V S P A R P A B B A T S L B G A L S G T R H S H P S V G R Q H H A G P T S R P P R P W D T P C P P V Y A S T K H F L Y S S G D K R Q L R P S F L L S SLTGARRL V STIFL 3 S R P W M P G T P R R L P Q R Y W Q ANTICOGCCCCTOTITICTOCAGCTGCTTGGGAACCACGCGGAGTGCCCCTACGGGGTSCTCTCAAGACGCACTGCCGGTGCGAGCTGCGGACCCCCAGCAGCCGCAGCAGCCGGTGTCTGTGCCCG м к р 1 р 1 в 1 1 6 м н а Q С Р У Б У 1 1 1 1 1 К Т н С Р 1 К А А У Т Р А А Б У С А К EKPQGSVAAPEZEDTDPRRLVQLLRQHSSPWQVYGFVRA L R R L V P P G L W G S R H N E R R ? L R N T K K P I S L G K H A K L S L Q E L GACGTGGAAGATGAGCGTCGGGGACTGCGCTTGGCTGCGCAGGAGCCCAGGGGTTGGCTTGTGTCCGGCCAAGAGCACCGTCTGCGTCAGGAGAATCCTGGCCAAGTTCCTGCACTGGCT TWKMSVRDCAWLRRS?3732VPAAEHRLREEILAKPLHWL I R Q H L K R V Q L A E L S E A 3 V R 3 H R E A R P A L L T S R L R F I P K P D V K V D V T G A Y D T I P Q D R L T B V I A S I I K P Q N T Y C V R R Y A V GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCAC KAAHGHVRKAPKSH GTCCTACGTCCAGTG G D P A G L H P L H A A L Q P V L R R H G E Q A V C G D S A G R A A P A F

TGATTTCTTGTTGACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCGAGGTGTCCCTGAGTATATGCCTGGTGAAGATGCGGAAGAACATTGCTGAACTTCCC

FIG. 11N

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ATGCCGCGCGCTCCCCGCTGCCGAGCCGTGCGCTCCCTGCTGCGCAGCCACTACCGCGAG MetProArgAlaProArgCysArgAlaValArgSerLeuLeuArgSerHisTyrArgGlu	60 20
GTGCTGCCGCTGGCCACGTTCGTGCGGCGCCTGGGGCCCCAGGGCTGGCGGCTGGTGCAG ValLeuProLeuAlaThrPheValArgArgLeuGlyProGlnGlyTrpArgLeuValGln	120 40
Valleurioneuriainirme vallagaesee-7	
CGCGGGGACCCGGCGGCTTTCCGCGCGCGCTGGTGGCCCAGTGCCTGGTGTGCGTGC	180 60

GACGCACGGCCGCCCCCCCCCCCCCTCCTTCCGCCAGGTG AspAlaArgProProProAlaAlaProSerPheArgGlnVal

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 $\tt CGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCAC$

GGCCTCCCCGGGGTCGGCGTCGGGGTTGAGGGCGGCGGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTG
G L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R F P R R
A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A G
P P R G R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q V

TCCTGCCTGAAGGAGCTG 240 SerCysLeuLysGluLeu 80	
GTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGCGCGAAGAACGTGCTGGCCTTCGGC	300
ValAlaArgValLeuGlnArgLeuCysGluArgGlyAlaLysAsnValLeuAlaPheGly	100
TTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGCCTTCACCACCAGCGTGCGC	360
PheAlaLeuLeuAspGlyAlaArgGlyGlyProProGluAlaPheThrThrSerValArg	120
Phearaneuneunsporyariamiggryory	
AGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGGGG	420
SerTyrLeuProAsnThrValThrAspAlaLeuArgGlySerGlyAlaTrpGlyLeuLeu	140
TTGCGCCGCGTGGGCGACGACGTGCTGGTTCACCTGCTGGCACGCTGCGCGCTCTTTGTG	480
LeuArgArgValGlyAspAspValLeuValHisLeuLeuAlaArgCysAlaLeuPheVal	160
CTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCCGCTGTACCAGCTCGGCGCT	540
LeuValAlaProSerCysAlaTyrGlnValCysGlyProProLeuTyrGlnLeuGlyAla	180
GCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAA	600
AlaThrGlnAlaArgProProHisAlaSerGlyProArgArgArgLeuGlyCysGlu	200
	660
CGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGGTCCCCCTGGGCCTGCCAGCCCCGGGT	220
ArgAlaTrpAsnHisSerValArgGluAlaGlyValProLeuGlyLeuProAlaProGly	220
	720
GCGAGGAGGCGCGGGGCAGTGCCAGCCGAAGTCTGCCCAAGAGGCCCAGGCGT	240
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GlyAlaAlaProGluProGluArgThrProValGlyGlnGlySerTrpAlaHisProGly	260
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GluAlaThrSerLeuGluGlyAlaLeuSerGlyThrArgHisSerHisProSerValGly	300
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CysProProValTyrAlaGluThrLysHisPheLeuTyrSerSerGlyAspLysGluGln	340
	1080
CTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGACTGGCGCTCGGAGGCTC	360
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GTGGAGACCATCTTTCTGGGTTCCAGGCCCTGGATGCCAGGGACTCCCCGCAGGTTGCCC	1140
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valuatintiliebuenengi Aberura rollibuen 1991 1991 1991 1991	

1200

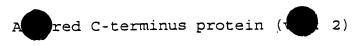
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CCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGTGGCGGCCCCCGAGGAG ProAlaAlaGlyValCysAlaArgGluLysProGlnGlySerValAlaAlaProGluGlu	1320 440
GAGGACACAGACCCCCGTCGCCTGGTGCAGCTGCTCCGCCAGCACAGCAGCCCCTGGCAGGCA	1380 460
GTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCCAGGCCTCTGGGGCTCC ValTyrGlyPheValArgAlaCysLeuArgArgLeuValProProGlyLeuTrpGlySer	1440 480
AGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCATCTCCCTGGGGAAGCAT ArgHisAsnGluArgArgPheLeuArgAsnThrLysLysPhelleSerLeuGlyLysHis	1500 500
GCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCGGGGCTGCGCTTGGCTG AlaLysLeuSerLeuGlnGluLeuThrTrpLysMetSerValArgAspCysAlaTrpLeu	1560 520
CGCAGGAGCCCAGGGGTTGGCTGTGTTCCGGCCGCAGAGCACCGTCTGCGTGAGGAGATC ArgArgSerProGlyValGlyCysValProAlaAlaGluHisArgLeuArgGluGluIle	1620 540
CTGGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTC LeuAlaLysPheLeuHisTrpLeuMetSerValTyrValValGluLeuLeuArgSerPhe	1680 560
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TGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGCAGCTGCGGGAG TrpSerLysLeuGlnSerIleGlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu	1800 600
CTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGCCAGGCCCGCCC	1860 620
CTCCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTG LeuArgPheIleProLysProAspGlyLeuArgProIleValAsnMetAspTyrValVal	1920 640
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CTGTTCAGCGTGCTCAACTACGAGCGGGGGGGCGCGCGCCCCGGCCTCTGTG LeuPheSerValLeuAsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAlaSerVal	2040 680
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•	
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•	
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SerLeuCysTyrSerTleLeuLySATabysAsimiraday	
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Interinted and a section of the sect	
CCGGCACTGCCCTCAGACTTCAAGACCATCCTGGAC	3420
ProAlaLeuProSerAspPheLysThrIleLeuAsp	1132
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PRAPRCZAVRS LLRSHTREV LPLAT F coececcae accecae acR R L G P Q G M R L V Q R G D P A A P R A L V A Q C L V C V P M D A R P P P GGCCTCCCCGGGGTCGGGTTCGGGTTGAGGGCGGCGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGCGACTCAGGGCGCTTCCCCCGCAGGTG L P G V G V R L G L R A A G G N Q R H A E S S A G D S G R P P R R A S P G S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A (P P R G R P A G V E G G R G E P A T C G E Q R R R L R A L P P Q PSFRQVSCLKELVARVLQRLCBRGAKNVLAFGFALLDGAR G G P P E A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D LVHLLARCALFVLVAPSCAYQVCGPPLYQLGAATQARP ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACCATAGGGTCAGGGAGGCCGGGGTCCCCTTGGGCCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGGCAGTGC HASGPRRLGCERAWNHS72BAGVPLGLPAPGARRGGSA RSLPLPKRPRRGAAPEP32°PVGQGSWAHPGRTRGPSDR G P C V V S P A R P A E S A T S L S G A L S G T R H S H P S V G R Q H H A G P P STSRPPRPWDTPCPPVYASTKHPLYSSGDKEQLRPSPLLS AATGCGGCCCCTGTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTACGGGGTSCTTCTTCAAGACGCACTGCCCGGTGCGGAGCTGCCGGAGCCGGTGCCCGAGCAGCCGGTGTCTGTGCCCG LFLELLGNHAQCPY3722KTHCPLRAAVTPAAGVCAR Z K P Q G S V A A P E E E D T D P R R L 7 Q L L R Q H S S P W Q V Y G F V R A C GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGGTGCGCAGGAGCCCAGGGGTTGGCTGTGTTGTTCCGGCGAAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGC T W K M S V R D C A W L R R S P G V G C V P A A E H R L R E E I L A K F L H W L I R Q H L K R V Q L R E L S S A E V R Q H R E A R P A L L T S R L R F I P K P D $\tt CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGGGTGCTCAACTACGA$ G L R P I V N M D Y V V G A R T ? R R Z X R A E R L T S R V K A L F S V L N Y E RARREGLE GASVEGED DE ARANTE VERVER VRAQDEPPEL GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA KAAHGHVRKAFKSHYSTLTDLQPYMRQFVAHLQETSPLRD TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTGAGAGCAGCAGAGCAGAGCAGAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGTCCTACGTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAAGGCAAGTCCTACGTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAAGGCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCAAGGCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCAAGGCCAA CCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCTGCAGCCTGTGCTACGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA Q G I P Q G S I L S T L L C S L C Y G D M B N K L F A G I R R D G L L L R L V TGTAGAAGACGAGGCCTGGGGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGGTGGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG V E D E A L G G T A F V Q M P A H G L F P M C G L L L D T R T L E V Q S D Y S R GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTCCTGCCGCCGCCTGTCCGCCCCTGCTGCGGGCAGGCGACTGCCAATCCCAAAGGGTCAGA ${\tt TGCCACAGGGTGCCCTCGTCCCATCTGGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTATTTTTGGTAA__$



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RAPZCZAVRSLLRSHTREVLPLATF W R L V Q R G D P A A P R A L V A Q C L V C V P W D A R P P P A A LGPQG GGCCTCCCCGGGTCGGCGTCGGGGTTGAGGGCGGCCGGGGAACCAGCGACATGCGGAGAGCAGGCGAGGCGACTCAGGGCGCTTCCCCCGGCAGGTG V G V R L G L R A A G G N Q R H A B S S A G D S G R P P R R ; S A S G W G * G R P G G T S D M R R A A Q A T Q G A S P A (LPGVGVRLGLRAAGGNQRHABSSAGDSGRPPR LPGVGVRLGLRAAGGNQRHABSSAGDSGRPPR ASPGSASGWG*GRPGGTSDMRRAAQATQGASP1 PPRGRPAGVBGGRGRPATCGEQRRRLRALPP SFRQVSCLKBLVARVLQRLCBRGAKNVLAFGFALLDGAR G G P P B A F T T S V R S Y L P N T V T D A L R G S G A W G L L L R R V G D D V GCTGGTTCACCTGCTGCCACGCTGCTGCGCGCTCTTTGTGCTGGTGGCTCCCAGGTGCGCCCTTACCAGGTGTGCGGGCCGCCGCTGTACCAGGTCGGCGCTGCCACTCAGGCCCGGGCCCCGGCC LVHLLARCALPVLVAPSCAYQVCGPPLYQLGAATQARPPP HAS GPRRLGCBRAWN HS VRZAGVPLGLPAPGARRGGSA CAGCCCAAGTCTGCCGTTGCCCAAGAGGCCCAGGCGTGCCCCTGAGCCGCAGGCCCGACGCCGGGCAGGACGCGTGGACCGAGTGACCG R S L P L P K R P R R G A A P E P 3 R T P V G Q G S W A H P G R T R G P S D R V S P A R P A B B A T S L 3 G A L S G T R H S H P S V G R Q H H A G P P AATGCGGCCCCTGTTTCTGGAACCACGCGCAGTGCCCCTACGGGTGCTCTCTCAAGACGCACTGCCCGGTGCGAGCTGCGGGTCACCCCAGCAGCCGGTGTCTGTGCCCG GACGTOGRAGATGAGCGTGCGGTTGGGTGCGCTGCGCGAGGGGGTTGGGTTAGGTTATGTTCCGGCCGCAGGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT T W K M S V R D C A W L R R S P G V 3 C V P A A E H R L R E E I L A K P L H W L GATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACACGCTCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGCTTGCAAAGCATTGG
M S V Y V V Z L L R S P Z Y V T Z T T Z Q K N R L F P Y R K S V W S K L Q S I G I R Q H L K R V Q L R S L S S A S V R Q B R S A S L R F L P K P $\tt CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGACAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA$ G L R P I V N M D Y V V G A R T F R R Z X R A E R L T S R V K A L P S V L N Y E GCGGGCGCGGCGCCCCGGCCTCCTGGGCGCCTTGTGCTGGGCCTTGGACGATATCCACAGGCCTTGGCGCCACCTTCGTGCTGCTGCTGCTGCGGCCCAGGACCCCGCCCCGCCTGAGCTGTACTT RARREGLIGASVIGLODIERARTEVLRVRAQDPPELYF R L T Z V I A S I I K P Q N T Y C V R R Y A V V GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACGTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA
K A A H G H V R K A F K S H V S T L T D L Q P Y M R Q F V A H L Q E T S P L R D TGTCAAG TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGGCAATGAGCCCAGGCCAGGCCAGGCCAGGCCGGCATCAGGGGCAAGTCCTACGTCCAGGCAATGAGGCCAGGCAGG Q G I P Q G S I L S T L L C S L C Y G D M 3 N K L P A G I R R D G L L R L V D TGATTTCTTGTTGGTGACACCTCACCCCACGCGAAAACCTTCCTCAGGACCCTGGTGGAGGTGTCCCTGAGTATGGCTGCGTGGAACTTGCGGAAGACAGTGGTGAACTTCCC L L V T P H L T H A K T P L R T L V R G V P S Y G C V V N L R K T V V N P P CTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGCCCAAACTCTTTGGGGTCTTGCGGCTGAAGTGTCACAGCCTGTTTCTGGA Y A R T S I R A S L T F N R G F K A 3 R N N R R K L F G V L R L K C H S L F L D TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA L Q V N S L Q T V C T N I Y K I L L L Q A Y R P H A C V L Q L P F H Q Q V W K N TPPLRVISDTASLCYSILKAKNAGMSLGAKGAAGPLPSE AVQWLCHQAPLLKLTRHRVTYVPLLGSLRTAQTQLSRKLP GAGTGTCCGGCTGAGGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGCCAGCTTTTCCTCAC CAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCCTCGCCCTCCTTTGCCTTCCACCCCCACCATCCAGGTGGAGACCCTGAGAA FIG. 11U

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PRAPRCRAVES LLRSHTREVLPLAT CONCRETE GROUP CONTRACTOR AND A R P P P A A R R L G P Q G W R L V Q R G D P A A P R A L V A Q C L V C V P W D A R P P P A A cccccctrcccccaractarccaractaracaractaractacaractaractacaractaractacaracta NUMBER AS GPRRLGGC BRAWNES V RS V RS V RLG LPAPGARRAGE TEGTTTCTGTGTGTGTCACCTGCCAGCCCGGAAGAAGCCACCTGTTTGGAGGCTGCGCCACGCGCCACCCCATCCGTGGGCCGCCAGCACCACGCGGGCCCCCC CTCTCTCAGGCCCAGCCTCACTGCGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGCGTTCCAGGCCCTGGATGCCAGGGATTCCCCGGAGGTTGCCCCGGAGGTTGCCCCGAGGGCTACTGGCA THE TRANSPORTED A R R L V E T I F L 3 S R P W M P G T P R R L P R L P Q R Y W Q GANGANGCCCCNGGGCTCTGTGGCGGCCCCCGNGGNGGAGGACACAGACCCCCGTCGCTGCTGCTGCAGCTGTCCGCCAGCACACAGCAGCCCCTTGGCAGGTGTACGGCTTCGTGCGGGCCTTG TOTACOTCOTCOAGCTCCTCAGGCCTCTTTTATGTCACGGAGACCACCTTTTTCTACCGGAAGAGTGTCTGGAGCAAGCTTGCAAAGCATTGC YVVELLRS?YYTETT?QKNRLF?YRKSVNSKLQSIG GOUCTGCGGCCGATTGTGAACATGGACTACGTCGTGKAACGCAGAACGTTCGCCAGAGAAAAAAAAAGAGGCCGAGCGTCCACCTCGAGGGTGAAGGCACTGTTCAGCGGGTGAAC G L R P I V N M D Y V V G A R T P R R R X R X E R L T S R V K A L P S V L N D R L T Z 7 : A S I I K P Q N T Y C V R R Y A V GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGCCGTTCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA K A A H G H V R K A P K S H V S T L T D L Q P Y M R Q P V A H L Q E T S P L R D TGATTTCTTGTTGGTGACACCTCACCTCACCCACGCGAAAAACCTTCCTCAGGACCCTGGTGCCCTGAGTATGGCTGCGTGAACTTGCGGAAGACAGTGGTGAACTTCCCC TGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGGTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG TOTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGATACC V S D E A L G G T A ? V Q M P A H G L ? ? M C G L L D T R T L E V Q S D Y GTGAGCGCACCTGGCCGGAAGTGGAGCCTGTGCCCGGCTGGGGCAGGTGCTGCTGCAGGGCCGTTTGCGTCCACCTCTGCTTCCGTGTGGGGCAGGCGACTGCCAAAGGGTCAGA

TGCCACAGGGTGCCCCTCGTCCCATCTGGGGCTGAGCACAAATGCATCTTTCTGTGGGAGTGAGGGTGCCTCACAACGGGAGCAGTTTTCTGTGCTAATTTTGGTAA

M P R A P R C R A V R S L L R S H T R E V L P L A T F V coecsectroscocccases coecsectroscocccs coecsectroscocccases coecsectroscocccases coecsectroscocccases coecsectroscoccases coecsectroscocccases coecsectroscoccases cRRLGPQGWRLVQRGDPAAFRALVAQCLVCVPWDARPPPAA $\tt Geccteccess Gate Gecate Gecate Gecate Gecate Gecate Gecate Gecate George Ge$ GRAPAGVEGERALE PPQ $\tt ccctrcttrccccaagatatcctgcctgaagacctgatgcccgaagacctgctgcagacccgaagacccgaagaacatgctggccttcggcttrccgctgcagacgggcccgaagaacatgctgcagacctgaagacctgcagaccagacccgaagaacatgctgcagaccagaccagacccgaagaacatgctgcagacca$ PSFRQVSCLKELVARVLQRLCBRGAKNVLAFGFALLDBRANGE BAFTTSVRSYLPNTVTDALRGSGAWGLLLRRVGDDV H L L A R C A L F V L V A P S C A Y Q V C G P P L Y Q L G A A T Q A R P P F ACACGCTAGTGGACCCCGAAGGCGTCTGGGATGCGAACGGGCCTGGAACGATAGCGTCAGGGAGGCCGGGGGTCCCCCTGGGCCTGCCAGCCCCGGGTGCGAGGACGCGGGGGGGAGTCC HASGPRRRLGCERAWNHSVRZAGVPLGLPAPGARRGGSA SRSLPLPKRPRRGAAPEPBRTPVGQGSWAHPGRTRGPSDR G F C V V S P A R P A B B A T S L E G A L S G T R H S H P S V G R Q H H A G P P STSRPPRPWDTPCPPVYASTKH?LYSSGDKEQLRPS?LLS S L R P S L T G A R R L V E T I P L G S R P M M P G T P R R L P R L P Q R Y W Q NATOCOGCCCCTOTTTCTGGAGCTGCTTGGGAACCACGCGCAGTGCCCCTTACGGGGTGCTCTCAAGACGCACTGCCGGTGCGAGCTGCGGTCACCCCGGTGCGAGCCGGTGCTGTGCCCG M R P L P L E L L G N H A Q C P Y G V L L K T H C P L R A A V T P A A G V C A R GACGTGGAAGATGAGCGTGCGGGACTGCGCTTGGGTGCGCAGGGGCCCAGGGGTTGGCTGTGTTTCCGGCCGAGAGCACCGTCTGCGTGAGGAGATCCTGGCCAAGTTCCTGCACTGGCT TWKMSVRDCAMELOCIAL RRSPGYGCYP λ λ EHRLRSSIL λ KFLH IRQHEKRYQLRELSEASYRD HREARFIPK PD $\tt CGGGCTGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGAGAAAAGAGGGCCGAGGGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCTCAACTACGA$ G L R P I V N M D Y V V G A R T P R R Z K R A Z R L T S R V K A L P S V L N 9CGGGCGCGGGGCCCCGGGCCTCTGTGCTGGGCCTGGACGATATCCACAGGCCTGGCGCACCTTCGTGCTGCGGGGCCCAGGACCCGCCGCCGCCTGAGCTGTACTT RARRPGLIGAS V LG LD DIHRAWRTPV LRVRAQ DPPP D R L T E 7 I A S I I K P Q N T Y C V R R Y A V TGTCAAG GAAGGCCGCCCATGGGCACGTCCGCAAGGCCTTCAAGAGCCACGTCTCTACCTTGACAGACCTTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAGACCAGCCCGCTGAGGGA KAAHGHVRKAPKSHVSTLTDIQPYMRQPVAHLQETSPLRD TGCCGTCGTCATCGAGCAGAGCTCCTCCCTGAATGAGGCCAGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATCAGGGGCAAGTCCTACGTCCAGTG VIEQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQC $\tt CCAGGGGATCCCGCAGGGCTCCATCCTCCACGCTGCTCTGCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTGCGGGGGATTCGGCGGGACGGGCTGCTCCTGCGTTTGGTGGA$ Q G I P Q G S I L S T L L C S L C Y G D M Z N K L F A G I R R D G L L L R L TGATTICTTGTTGGTGACACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGAGTTGCGGAAGACAGTGGTGAACTTCCCC
D F L L V T P H L T H A K T F L R T L V R G V P E Y G C V V N L R K T V V N P P TGTAGAAGACGAGGCCTGGGTGGCACGGCTTTTGTTCAGATGCCGGCCCACGGCCTATTCCCCTGGTGCGGCCTGCTGCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAG V E D E A L G G T A F V Q M P A H G L F P W C G L L D T R T L E V Q S D Y S S Y A R T S I R A S L T P N R G P K A G R N M R R K L P G V L R L K C H S L P L D TTTGCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCACGCATGTGTGCTGCAGCTCCCATTTCATCAGCAAGTTTGGAAGAA LQVNSLQTVCTNIYKILLLQAYRFHACVLQLPFHQQV $\tt CCCCACATTTTTCCTGCGCGTCATCTCTGACACGGCCTCCCTTGCTACTCCATCCTGAAAGCCAAGAACGCAGGGATGTCGCTGGGGGCCAAGGGCCCCCGGCCCTCTGCCCTCCGA$ PTPPLRVISDTASCULAR CCGAAGAAAACATTTCTGTCGTGACTCCTGCGGTGCTTGGGTC E E N I L V V T P A V L G S

And the state of t

FIG. 12

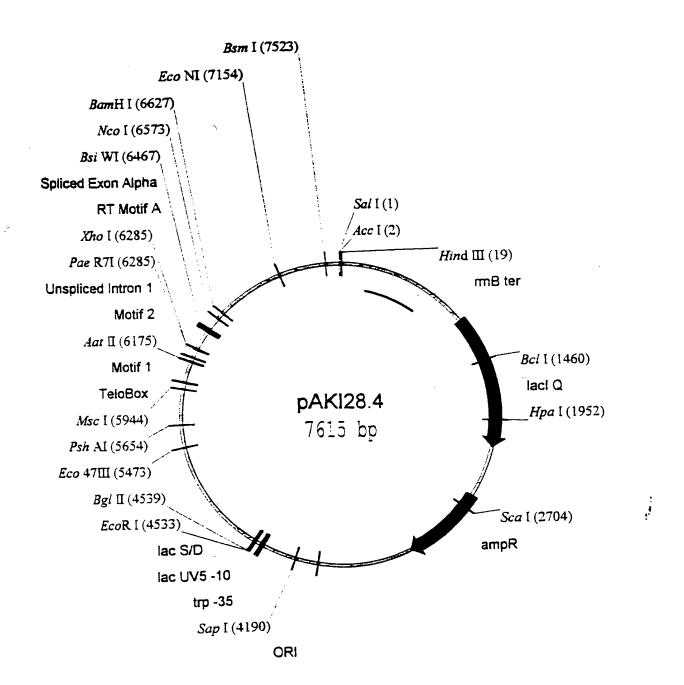


FIG. 13A

LOCUS pAKI28.4 7615 bp dsDNA Circular DEFINITION Human telomerase clone with exon beta spliced out

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1 tegacetgea ggeatgeaag ettggeactg geegtegttt tacaacgteg tgactgggaa 61 aaceetggeg ttacecaact taategeett geageacate eccettege eagetggegt 121 aatagegaag aggeeegeac egategeest teecaacagt tgegeageet gaatggegaa 181 tggegeetga tgeggatgat teteettaeg eatetgtgeg gtattteaca eegeataaat 241 teeetgttt ggeggatgag agaagatttt eageetgata eagataaat eagaacgeag 301 aageggtetg ataaaacaga atttgeetgg eggeagtage geggtggtee eacetgaece 361 eatgeegaac teagaagtga aacgeegtag eggeagtggt agtgtggggt eteeceatge 421 gagagtaggg aactgeeagg eateaaataa aacgaaagge teagtegaaa gactgggeet 481 ttegttttat etgttgtttg teggtgaacg eteteetgag taggacaaaat eegeegggag 541 eggattgaa egttgegaag eaacggeeeg gagggtggeg ggeaggaege eegeeataaa 601 etgeeaggaa teaaattaag eagaaggeea teetgaegga tggeettttt gegtttetae 661 aaactettee tgtegteata tetacaagee ateeeeceae agatacagta aactageete 721 gtttttgeat eaggaaagee eggaaatttat ggtgeactet eagtacaate tgetetgatg 781 eegeatagtt aageeageee egacaceege eaacaceege tgaeggeee tgaeggeet
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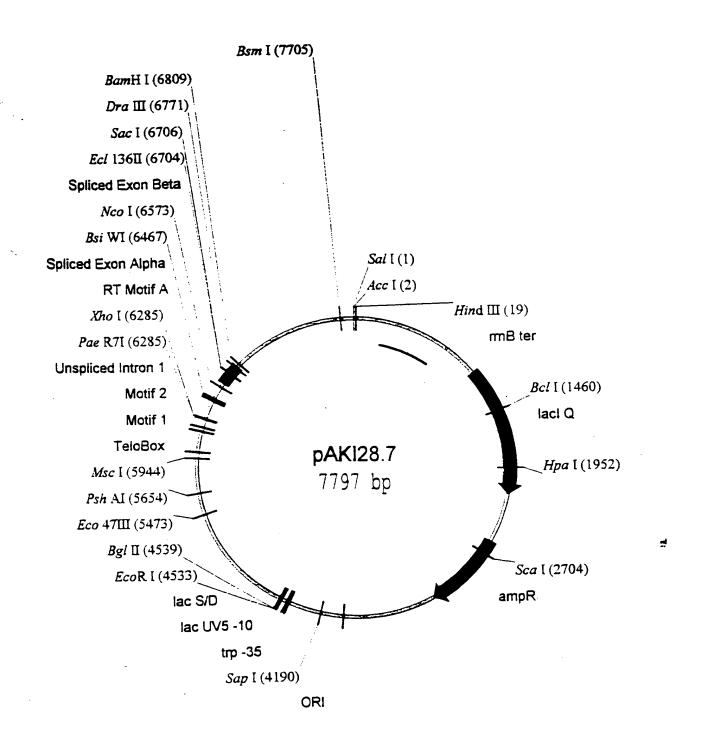


FIG. 14A

LOCUS pAKI28.7 7797 bp dsDNA Circular DEFINITION Human telomerase clone with alternative C-terminus

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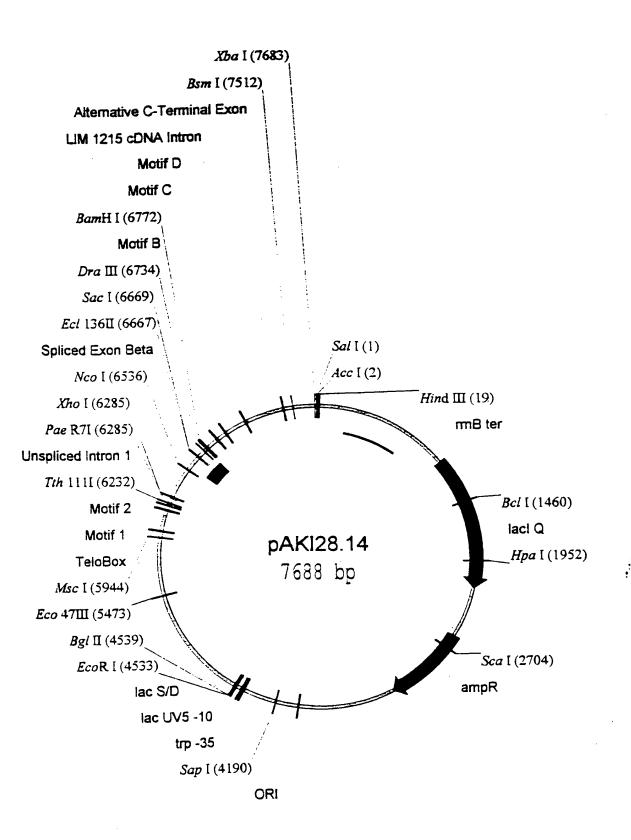
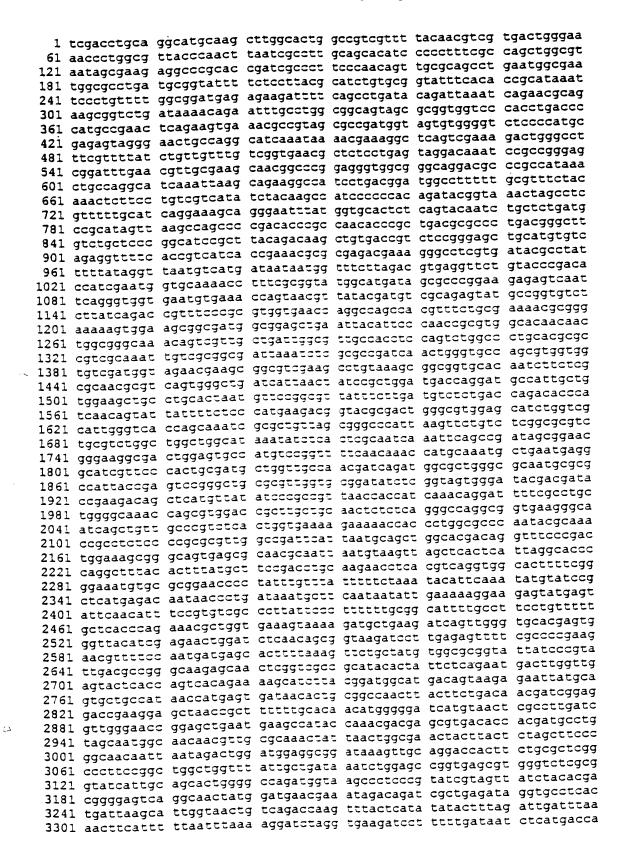


FIG. 15A

LOCUS pAKI28.14 7688 bp dsDNA Circular DEFINITION Human telomerase clone with exon alpha spliced out



3361 aaatccctta acqtgagttt tcgttccact gagcgtcaga ccccgtagaa aagatcaaag 3421 gatettettg agateetttt tttetgegeg taatetgetg ettgeaaaca aaaaaaceae 3481 cgctaccage ggtggtttgt ttgccggate aagagetace aactettttt ccgaaggtaa 3541 ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg tagttaggcc 3601 accaetteaa gaaetetgta geaeegeeta eataeetege tetgetaate etgttaeeag 3661 tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga cgatagttac 3721 cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc agcttggagc 3781 gaacqaccta caccgaactg agatacctac agcgtgagca ttgagaaagc gccacgcttc 3841 ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca ggagagcgca 3901 cgagggaget tecaggggga aacgeetggt atetttatag teetgteggg tttegeeace 3961 tetqaettqa gegtegattt ttgtgatget egteaggggg geggageeta tggaaaaaeg 4021 ccagcaacgc ggccttttta cggttsctgg ccttttgctg gccttttgct cacatgttct 4081 ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag tgagctgata 4141 ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa gcggaagagc 4201 gcccaatacg caaaccgcct ctccccgcgc gttggccgat tcattaatgc agaattaatt 4261 ctcatgtttg acagcttatc atcgactgca cggtgcacca atgcttctgg cgtcaggcag 4321 ccatcggaag ctgtggtatg gctgtgcagg tcgtaaatca ctgcataatt cgtgtcgctc 4381 aaggcgcact cccgttctgg ataatgtttt ttgcgccgac atcataacgg ttctggcaaa 4441 tattctgaaa tgagctgttg acaattaatc atcggctcgt ataatgtgtg gaattgtgag 4501 cggataacaa tttcacacag gaaacagcga tgaattcaga tctcaccatg aaggagctgg 4561 tggcccqagt gctgcagagg stgtgcgagc gcggcgcgaa gaacgtgctg gcsttcggct 4621 tegegetget ggaeggggee egegggggee ecceegagge etteaceace agegtgegea 4681 gctacctgcc caacacggtg accgacgcac tgcgggggag cggggcgtgg gggctgctgc 4741 tgcgccgcgt gggcgacgac gtgctggttc acctgctggc acgctgcgcg ctctttgtgc 4801 tggtggctcc cagctgcgcc taccaggtgt gcgggccgcc gctgtaccag ctcggcgctg 4861 ccactcagge eeggeeeeg ccacaegeta gtggaeeeeg aaggegtetg ggatgegaae 4921 gggcctggaa ccatagcgtc agggaggccg gggtccccct gggcctgcca gccccgggtg 4981 cgaggaggc cgggggcagt gccagccgaa gtctgccgtt gcccaagagg cccaggcgtg 5041 qcqctqcccc tgagccggag cggacgcccg ttgggcaggg gtcctgggcc cacccgggca 5101 ggacgcgtgg accgagtgac cgtggtttct gtgtggtgtc acctgccaga cccgccgaag 5161 aagecacete tttggagggt gegetetetg geaegegeea eteceaecea teegtgggee 5221 gecageacea egegggeece ceatecaeat egeggeeace aegteeetgg gaeaegeett 5281 gtcccccggt gtacgccgag accaagcact tcctctactc ctcaggcgac aaggagcagc 5341 tgcggcctc cttcctactc agctctctga ggcccagcct gactggcgct cggaggctcg 5401 tggagaccat etttetgggt tesaggesst ggatgesagg gastessege aggttgesse 5461 gcctgcccca gcgctactgg caaatgcggc ccctgtttct ggagctgctt gggaaccacg 5521 cgcagtgccc ctacggggtg ctcctcaaga cgcactgccc gctgcgagct gcggtcaccc 5581 cagcageegg tgtetgtgee egggagaage eecagggete tgtggeggee eecgaggagg 5641 aggacacaga ecceegtege etggtgeage tgeteegeea geacageage ecetggeagg 5701 tgtacggett egtgegggee tgeetgegee ggetggtgee eccaggeete tggggeteea 5761 ggcacaacga acgccgcttc ctcaggaaca ccaagaagtt catctccctg gggaagcatg 5821 ccaaqctctc gctgcaggag ctgacgtgga agatgagcgt gcgggactgc gcttggctgc 5881 gcaggagece aggggttgge tgtgtteegg eegeagagea eegtetgegt gaggagatee 5941 tggccaagtt cotgcactgg ctgatgagtg tgtacgtcgt cgagctgctc aggtctttct 6001 tttatqtcac ggagaccacg tttcaaaaaga acaggctctt tttctaccgg aagagtgtct 6061 ggagcaagtt gcaaagcatt ggaatsagac agcacttgaa gagggtgcag ctgcgggagc 6121 tgtcggaagc agaggtcagg cagcatcggg aagccaggec cgccctgctg acgtccagac 6181 teagetteat ecceaageet gacgggetge ggeogattgt gaacatggae tacgtegtgg 6241 gagccagaac gttccgcaga gaaaagaggg ccgagcgtct cacctcgagg gtgaaggcac 6301 tgttcagcgt gctcaactac gagcgggcgc ggcgccccgg cctcctgggc gcctctgtgc 6361 tgggcctgga cgatatccac agggcctggc gcaccttcgt gctgcgtgtg cgggcccagg 6421 accegeegee tgagetgtae tttgteaagg acaggeteae ggaggteate gecageatea 6481 tcaaacccag aacacgtact gcgtgcgtcg gtatgccgtg gtccagaagg ccgcccatgg 6541 gcacqtccqc aaggccttca agagccacqt ctctaccttg acagacctcc agccgtacat 6601 gcgacagttc gtggctcacc tgcaggagac cagcccgctg agggatgccg tcgtcatcga 6661 gcagagetee tecetgaatg aggesageag tggeetette gaegtettee taegetteat 6721 gtgccaccac gccgtgcgca tcaggggcaa gtcctacgtc cagtgccagg ggatcccgca

